

SEQUENCE LISTING

JUL 20 1998

(1) GENERAL INFORMATION:

- (i) APPLICANT: Muller-Rober, Bernd
Land-Schutze, Volker
La Cognata, Ursula
- (ii) TITLE OF INVENTION: PROCESSES FOR INHIBITING AND FOR
INDUCING FLOWER FORMATION IN PLANTS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DCS/MS-DCS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/702,718
(B) FILING DATE: 19-MAR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE P4408629.6
(B) FILING DATE: 09-MAR-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE P4435366.9
(B) FILING DATE: 22-SEP-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE P4438821.7
(B) FILING DATE: 19-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: AGREVO-1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-596-9000
(B) TELEFAX: 212-596-9090

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Solanum tuberosum
 (B) STRAIN: c.v. Desiree
 (F) TISSUE TYPE: leaf
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA library in pBluescriptKS
 (B) CLONE: pCBS
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 73..1485
 (D) OTHER INFORMATION: /EC_number= 4.1.3.7.
 /product= "Citrate synthase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTCGTTT	CATCAGCCTA	CTTGAGATGT	ATTCCCACTG	GTAAAAGTTA	ATTTTTTTGA	60
TTTTTCGCGAG	CA ATG GTG TTC TAC CGT AGC GTT TCG TTG CTG TCA AAG	108				
	Met Val Phe Tyr Arg Ser Val Ser Leu Leu Ser Lys					
	1 5 10					
CTC CGC TCT CGA GCG GTC CAA CAG TCA AAT GTT AGC AAT TCT GTG CGC	156					
Leu Arg Ser Arg Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg						
	15 20 25					
TGG CTT CAA GTC CAA ACC TCT TCC GGT CTT GAT CTG CGT TCT GAG CTG	204					
Trp Leu Gln Val Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu						
	30 35 40					
GTA CAA GAA TTG ATT CCT GAA CAA CAG GAT CGC CTG AAA AAG ATC AAG	252					
Val Gln Glu Leu Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Ile Lys						
	45 50 55 60					
TCA GAT ATG AAA GGT TCA ATT GGG AAC ATC ACA GTT GAT ATG GTT CTT	300					
Ser Asp Met Lys Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu						
	65 70 75					
GGT GGA ATG AGA GGA ATG ACA GGA TTA CTG TGG AAA CCT CAT TAC CTT	348					
Gly Gly Met Arg Gly Met Thr Gly Leu Leu Trp Lys Pro His Tyr Leu						
	80 85 90					
GAC CCT GAT GAG GGA ATT CGC TTC CGG GGG TTG TCT ATA CCT GAA TGC	396					
Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys						
	95 100 105					
CAA AAG GTA TTA CCT GCA GCA AAG CCT GGG GGT GAG CCC TTG CCT GAA	444					
Gln Lys Val Leu Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu						
	110 115 120					
GGT CTT CTC TGG CTT CTT TTA ACA GGA AAG GTG CCA TCA AAA GAG CAA	492					
Gly Leu Leu Trp Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln						
	125 130 135 140					

GTG AAT TCA ATT GTC TCA GGA ATT GCA GAG TCG GGC ATC ATA TCC CTG Val Asn Ser Ile Val Ser Gly Ile Ala Glu Ser Gly Ile Ile Ser Leu 145 150 155	540
ATC ATC ATG TAT ACA ACT ATT GAT GCC TTA CCA GTC ACA GCT CAT CCA Ile Ile Met Tyr Thr Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro 160 165 170	588
ATG ACC CAG TTT GCT ACT GGA GTC ATG GCT CTT CAG GTT CAA AGT GAA Met Thr Gln Phe Ala Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu 175 180 185	636
TTT CAA AAG GCA TAC GAG AAA GGG ATT CAC AAA TCA AAG TAT TGG GAA Phe Gln Lys Ala Tyr Glu Lys Gly Ile His Lys Ser Lys Tyr Trp Glu 190 195 200	684
CCA ACA TAT GAG GAT TCC ATG AAT CTG ATT GCT CAA GTT CCA CTT GTT Pro Thr Tyr Glu Asp Ser Met Asn Leu Ile Ala Gln Val Pro Leu Val 205 210 215 220	732
GCT GCT TAT GTT TAT CGC AGG ATG TAC AAG AAT GGT GAC ACT ATA CCT Ala Ala Tyr Val Tyr Arg Arg Met Tyr Lys Asn Gly Asp Thr Ile Pro 225 230 235	780
AAG GAT GAA TCC CTG GAT TAT GGT GCA AAT TTT GCT CAC ATG CTT GGT Lys Asp Glu Ser Leu Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly 240 245 250	828
TTC AGT AGC TCT GAA ATG CAT GAA CTT CTT ATG AGG CTC TAT GTA ACA Phe Ser Ser Ser Glu Met His Glu Leu Leu Met Arg Leu Tyr Val Thr 255 260 265	876
ATA CAC AGT GAT CAT GAA GGT GGT AAT GTC AGT GCT CAC ACC GGT CAC Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala His Thr Gly His 270 275 280	924
TTG GTT GCT AGT GCT TTG TCT GAT CCT TAC CTC TCC TTT GCT GCT GCT Leu Val Ala Ser Ala Leu Ser Asp Pro Tyr Leu Ser Phe Ala Ala Ala 285 290 295 300	972
TTG AAT GGT TTA GCC GGA CCA CTT CAT GGT TTA GCC AAT CAG GAA GTT Leu Asn Gly Leu Ala Gly Pro Leu His Gly Leu Ala Asn Gln Glu Val 305 310 315	1020
TTG CTA TGG ATA AAA TCT GTT GTA GAA GAA TGT GGG GAG AAC ATT TCC Leu Leu Trp Ile Lys Ser Val Val Glu Glu Cys Gly Glu Asn Ile Ser 320 325 330	1068
AAA GAG CAG TTG AAA GAC TAT GTT TGG AAA ACA TTG AAC AGT GGC AAG Lys Glu Gln Leu Lys Asp Tyr Val Trp Lys Thr Leu Asn Ser Gly Lys 335 340 345	1116
GTT GTC CCT GGT TTT GGA CAT GGA GTT CTG CGA AAG ACT GTA CCA AGA Val Val Pro Gly Phe Gly His Gly Val Leu Arg Lys Thr Val Pro Arg 350 355 360	1164
TAT ACA TGC CAG AGA GAG TTC GCT ATG AAG CAT TTG CCT GAA GAT CCA Tyr Thr Cys Gln Arg Glu Phe Ala Met Lys His Leu Pro Glu Asp Pro 365 370 375 380	1212

CTG TTT CAA CTG GTT TCA AAA CTC TAC GAA GTT TTC CTC CTG TTC TTA Leu Phe Gln Leu Val Ser Lys Leu Tyr Glu Val Phe Leu Leu Phe Leu 385 390 395	1260
CAG AAC TTG GCA AAG TTA AAA CCT TGG CCA AAT GTT GAT GCC CAC AGT Gln Asn Leu Ala Lys Leu Lys Pro Trp Pro Asn Val Asp Ala His Ser 400 405 410	1308
GGT GTG TTG TTG AAC TAT TAT GGT TTA ACT GAA GCA AGA TAT TAT ACG Gly Val Leu Leu Asn Tyr Tyr Gly Leu Thr Glu Ala Arg Tyr Tyr Thr 415 420 425	1356
GTC CTC TTT GGC GTA TCA AGA GCT CTT GGC ATT TGC TCT CAG CTA ATT Val Leu Phe Gly Val Ser Arg Ala Leu Gly Ile Cys Ser Gln Leu Ile 430 435 440	1404
TGG GAC CGA GCT CTT GGA TTG CCG CTA GAG AGG CCA AAG AGT GTC ACA Trp Asp Arg Ala Leu Gly Leu Pro Leu Glu Arg Pro Lys Ser Val Thr 445 450 455 460	1452
ATG GAG TGG CTT GAG AAC CAG TGC AAG AAA GCA TGAATTGTTT GAAATCTCGC Met Glu Trp Leu Glu Asn Gln Cys Lys Lys Ala 465 470	1505
GAGCATAAAA CACAATGTAT AATCTCTATG AATAATTGCT TGACAAAGCA CTCCTTTCTT	1565
GGGGGACAAG ATAGGTCGGC CCTTCAATGG GTTAACGAAC TTCAGTTCAA ACTTCACTGA	1625
ATTTGTGTGA ATTGTATGGT TTCTCGAGAC TTGTCCTGAA TTTTGAACCT AGTCTAGTGG	1685
ATTCATTTTT CTTCATTCCG AATTCCTCAC ACGCTGATCC AGCATGTAAA AATTAATAGG	1745
TCAATGCTAT TAATCGCGTT CTTGGTTGCC ATTAGACTTG TGAATGACTT CCTTTGCTGG	1805
AAAGTTAGTA ATCGGCTGAT TCACGCAATA AACTGCAATT GTGTAGTTTC TTAAATTTGC	1865
TAATTCTTAT TTGATGATAT TATGAA	1891

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Phe Tyr Arg Ser Val Ser Leu Leu Ser Lys Leu Arg Ser Arg 1 5 10 15
Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg Trp Leu Gln Val 20 25 30
Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu Val Gln Glu Leu 35 40 45
Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Ile Lys Ser Asp Met Lys 50 55 60

Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Met Arg
65 70 75 80

Gly Met Thr Gly Leu Leu Trp Lys Pro His Tyr Leu Asp Pro Asp Glu
85 90 95

Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys Gln Lys Val Leu
100 105 110

Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu Gly Leu Leu Trp
115 120 125

Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asn Ser Ile
130 135 140

Val Ser Gly Ile Ala Glu Ser Gly Ile Ile Ser Leu Ile Ile Met Tyr
145 150 155 160

Thr Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro Met Thr Gln Phe
165 170 175

Ala Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu Phe Gln Lys Ala
180 185 190

Tyr Glu Lys Gly Ile His Lys Ser Lys Tyr Trp Glu Pro Thr Tyr Glu
195 200 205

Asp Ser Met Asn Leu Ile Ala Gln Val Pro Leu Val Ala Ala Tyr Val
210 215 220

Tyr Arg Arg Met Tyr Lys Asn Gly Asp Thr Ile Pro Lys Asp Glu Ser
225 230 235 240

Leu Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly Phe Ser Ser Ser
245 250 255

Glu Met His Glu Leu Leu Met Arg Leu Tyr Val Thr Ile His Ser Asp
260 265 270

His Glu Gly Gly Asn Val Ser Ala His Thr Gly His Leu Val Ala Ser
275 280 285

Ala Leu Ser Asp Pro Tyr Leu Ser Phe Ala Ala Ala Leu Asn Gly Leu
290 295 300

Ala Gly Pro Leu His Gly Leu Ala Asn Gln Glu Val Leu Leu Trp Ile
305 310 315 320

Lys Ser Val Val Glu Glu Cys Gly Glu Asn Ile Ser Lys Glu Gln Leu
325 330 335

Lys Asp Tyr Val Trp Lys Thr Leu Asn Ser Gly Lys Val Val Pro Gly
340 345 350

Phe Gly His Gly Val Leu Arg Lys Thr Val Pro Arg Tyr Thr Cys Gln
355 360 365

Arg Glu Phe Ala Met Lys His Leu Pro Glu Asp Pro Leu Phe Gln Leu
370 375 380

Val Ser Lys Leu Tyr Glu Val Phe Leu Leu Phe Leu Gln Asn Leu Ala
385 390 395 400

Lys Leu Lys Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu
405 410 415
Asn Tyr Tyr Gly Leu Thr Glu Ala Arg Tyr Tyr Thr Val Leu Phe Gly
420 425 430
Val Ser Arg Ala Leu Gly Ile Cys Ser Gln Leu Ile Trp Asp Arg Ala
435 440 445
Leu Gly Leu Pro Leu Glu Arg Pro Lys Ser Val Thr Met Glu Trp Leu
450 455 460
Glu Asn Gln Cys Lys Lys Ala
465 470

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1551 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Beta vulgaris
 - (B) STRAIN: Zuchtlinie 5S 0026
 - (F) TISSUE TYPE: leaf
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pSBCS
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1311
 - (D) OTHER INFORMATION: /EC_number= 4.1.3.7.
/product= "citrate synthase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCC TCT AAC CTT GAC CTT CGT TCA GAG TTA CAA GAA CTG ATT CCT GAA	48
Ser Ser Asn Leu Asp Leu Arg Ser Glu Leu Gln Glu Leu Ile Pro Glu	15
1 5 10	
CAA CAG GAA CGA CTG AAG AAG ATA AAG AAA GAA TTT GGA AGT TTC CAG	96
Gln Gln Glu Arg Leu Lys Lys Ile Lys Lys Glu Phe Gly Ser Phe Gln	30
20 25 30	
CTG GGG AAT ATC AAT GTT GAC ATG GTA TTG GGC GGA ATG AGA GGA ATG	144
Leu Gly Asn Ile Asn Val Asp Met Val Leu Gly Gly Met Arg Gly Met	45
35 40 45	
ACT GGT TTA CTT TGG GAG ACT TCC TTA CTC GAC CCA GAA GAG GGT ATC	192
Thr Gly Leu Leu Trp Glu Thr Ser Leu Leu Asp Pro Glu Glu Gly Ile	60
50 55 60	
CGG TTC AGG GGT TTT TCT ATA CCT GAA TGC CAG AAA CTT TTA CCC GCT	240
Arg Phe Arg Gly Phe Ser Ile Pro Glu Cys Gln Lys Leu Leu Pro Ala	75 80
65 70 75 80	

GCA AGT GCT GGT GCA GAG CCA TTG CCT GAA GGT CTT CTT TGG CTT CTT Ala Ser Ala Gly Lys Ala Glu Pro Leu Pro Glu Gly Leu Leu Trp Leu Leu	288
85 90 95	
TTA ACC GGA AAG GTT CCT AGC AAA GAG CAA GTA GAT GCT CTA TCA GCA Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ala Leu Ser Ala	336
100 105 110	
GAT TTA CGA AAA CGT GCT TCT ATC CCA GAC CAT GTG TAC AAA ACA ATT Asp Leu Arg Lys Arg Ala Ser Ile Pro Asp His Val Tyr Lys Thr Ile	384
115 120 125	
GAT GCT CTA CCT ATT ACG GCT CAT CCA ATG ACT CAG TTT TGC ACT GGT Asp Ala Leu Pro Ile Thr Ala His Pro Met Thr Gln Phe Cys Thr Gly	432
130 135 140	
GTT ATG GCC TTA CAG ACT CGA AGC GAA TTT CAG AAG GCA TAT GAG AAA Val Met Ala Leu Gln Thr Arg Ser Glu Phe Gln Lys Ala Tyr Glu Lys	480
145 150 155 160	
GGG ATC CAT AAG TCA AAG TTT TGG GAG CCA ACA TAT GAG GAC TGC CTT Gly Ile His Lys Ser Lys Phe Trp Glu Pro Thr Tyr Glu Asp Cys Leu	528
165 170 175	
AGT TTG ATT GCT CAA GTT CCT GTT GTT GCA GCT TAT GTT TAT CGG AGG Ser Leu Ile Ala Gln Val Pro Val Val Ala Ala Tyr Val Tyr Arg Arg	576
180 185 190	
ATG TAT AAG AAT GGA CAA GTA ATA CCG CTG GAT GAC TCC CTT GAT TAT Met Tyr Lys Asn Gly Gln Val Ile Pro Leu Asp Asp Ser Leu Asp Tyr	624
195 200 205	
GGT GGA AAT TTC GCA CAC ATG TTG GGA TTT GAT AGC CCT CAG ATG CTT Gly Gly Asn Phe Ala His Met Leu Gly Phe Asp Ser Pro Gln Met Leu	672
210 215 220	
GAG CTG ATG CGC CTT TAT GTC ACA ATT CAC AGT GAT CAT GAG GGT GGA Glu Leu Met Arg Leu Tyr Val Thr Ile His Ser Asp His Glu Gly Gly	720
225 230 235 240	
AAT GTT AGT GCA CAC ACT GGC CAT TTG GTG GGT AGT CCA CTT TCA GAT Asn Val Ser Ala His Thr Gly His Leu Val Gly Ser Pro Leu Ser Asp	768
245 250 255	
CCT TAT TTG TCA TTT GCA GCA GCA TTA AAT GGT TTG GCT GGG CCA CTC Pro Tyr Leu Ser Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly Pro Leu	816
260 265 270	
CAT GGA TTA GCC AAC CAG GAA GTC CTG CTG TGG ATT AAA TCA GTT GTT His Gly Leu Ala Asn Gln Glu Val Leu Leu Trp Ile Lys Ser Val Val	864
275 280 285	
GAT GAA TGT GGA GAG AAC ATC TCG ACA GAG CAG TTG AAA GAT TAT GTT Asp Glu Cys Gly Glu Asn Ile Ser Thr Glu Gln Leu Lys Asp Tyr Val	912
290 295 300	
TGG AAG ACA CTA AAC AGT GGC AAG GTT GTA CCT GGA TTT GGT CTA GGA Trp Lys Thr Leu Asn Ser Gly Lys Val Val Pro Gly Phe Gly Leu Gly	960
305 310 315 320	

GTA TTG CGG AAG ACA GAT CCA AGA TAC ACA TGC CAA AGA GAA TTT GCG Val Leu Arg Lys Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu Phe Ala 325 330 335	1008
TTG AAG CAC TTG CCT GAT GAC CCA TTT TTT CAA TTG GTG TCA AAG TTG Leu Lys His Leu Pro Asp Asp Pro Phe Phe Gln Leu Val Ser Lys Leu 340 345 350	1056
TAT GAA GTG GTG CCT CCT ATT CTA TTA GAG CTT GGA AAG GTA AAG AAT Tyr Glu Val Val Pro Pro Ile Leu Leu Glu Leu Gly Lys Val Lys Asn 355 360 365	1104
CCA TGG CCT AAT GTT GAT GCT CAT AGT GGA GTT TTG CTG AAC CAC TAT Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu Asn His Tyr 370 375 380	1152
GGT TTG ACA GAA GCA AGA TAC TAT ACG GTT TTG TTT GGG GTA TCA AGG Gly Leu Thr Glu Ala Arg Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg 385 390 395 400	1200
AGT CTT GGA ATA TGC TCA CAG CTT ATA TGG GAC CGA GCT CTT GGC TTG Ser Leu Gly Ile Cys Ser Gln Leu Ile Trp Asp Arg Ala Leu Gly Leu 405 410 415	1248
CCG CTA GAG AGG CCA AAG AGT GTC ACT ATG GAA TGG CTT GAA AAG TTT Pro Leu Glu Arg Pro Lys Ser Val Thr Met Glu Trp Leu Glu Lys Phe 420 425 430	1296
TGT AAA AGA AGA GCA TA ACATTGATGA CATATCAACT CACTGTTGTT Cys Lys Arg Arg Ala 435	1343
CTTTGTCGAA TCTACAATAA TATAGTTTGA GGGACAAGAA AGAATTTTAT TTTCGGAGAT	1403
GAGATAAGCG AGGACTCAGA AACATAGTTT TCTTTGTCTC TTGCTGAGGT TTGCGTTTTA	1463
TATATTTTAC TTGTAAATAT ATTGTATGGT TTCTTGATCA AAACATGAGA TAAAGAGTTT	1523
TCATAAAAAA AAAAAAAAAA AAAAAAAAAA	1551

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ser Asn Leu Asp Leu Arg Ser Glu Leu Gln Glu Leu Ile Pro Glu 1 5 10 15
Gln Gln Glu Arg Leu Lys Lys Ile Lys Lys Glu Phe Gly Ser Phe Gln 20 25 30
Leu Gly Asn Ile Asn Val Asp Met Val Leu Gly Gly Met Arg Gly Met 35 40 45

Thr Gly Leu Leu Trp Glu Thr Ser Leu Leu Asp Pro Glu Glu Gly Ile
50 55 60

Arg Phe Arg Gly Phe Ser Ile Pro Glu Cys Gln Lys Leu Leu Pro Ala
65 70 75 80

Ala Ser Ala Gly Ala Glu Pro Leu Pro Glu Gly Leu Leu Trp Leu Leu
85 90 95

Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ala Leu Ser Ala
100 105 110

Asp Leu Arg Lys Arg Ala Ser Ile Pro Asp His Val Tyr Lys Thr Ile
115 120 125

Asp Ala Leu Pro Ile Thr Ala His Pro Met Thr Gln Phe Cys Thr Gly
130 135 140

Val Met Ala Leu Gln Thr Arg Ser Glu Phe Gln Lys Ala Tyr Glu Lys
145 150 155 160

Gly Ile His Lys Ser Lys Phe Trp Glu Pro Thr Tyr Glu Asp Cys Leu
165 170 175

Ser Leu Ile Ala Gln Val Pro Val Val Ala Ala Tyr Val Tyr Arg Arg
180 185 190

Met Tyr Lys Asn Gly Gln Val Ile Pro Leu Asp Asp Ser Leu Asp Tyr
195 200 205

Gly Gly Asn Phe Ala His Met Leu Gly Phe Asp Ser Pro Gln Met Leu
210 215 220

Glu Leu Met Arg Leu Tyr Val Thr Ile His Ser Asp His Glu Gly Gly
225 230 235 240

Asn Val Ser Ala His Thr Gly His Leu Val Gly Ser Pro Leu Ser Asp
245 250 255

Pro Tyr Leu Ser Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly Pro Leu
260 265 270

His Gly Leu Ala Asn Gln Glu Val Leu Leu Trp Ile Lys Ser Val Val
275 280 285

Asp Glu Cys Gly Glu Asn Ile Ser Thr Glu Gln Leu Lys Asp Tyr Val
290 295 300

Trp Lys Thr Leu Asn Ser Gly Lys Val Val Pro Gly Phe Gly Leu Gly
305 310 315 320

Val Leu Arg Lys Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu Phe Ala
325 330 335

Leu Lys His Leu Pro Asp Asp Pro Phe Phe Gln Leu Val Ser Lys Leu
340 345 350

Tyr Glu Val Val Pro Pro Ile Leu Leu Glu Leu Gly Lys Val Lys Asn
355 360 365

Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu Asn His Tyr
370 375 380

Gly Leu Thr Glu Ala Arg Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg
 385 390 395 400
 Ser Leu Gly Ile Cys Ser Gln Leu Ile Trp Asp Arg Ala Leu Gly Leu
 405 410 415
 Pro Leu Glu Arg Pro Lys Ser Val Thr Met Glu Trp Leu Glu Lys Phe
 420 425 430
 Cys Lys Arg Arg Ala
 435

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Nicotiana tabacum
 (F) TISSUE TYPE: leaf

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: TCS

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 70..1476
 (D) OTHER INFORMATION: /EC_number= 4.1.3.7.
 /product= "citrate synthase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTCTTGGA TCTATTCCT CTCTCTATTT CTCCTAGGT AAAAGTTAAT TTGTTGATT 60
 TTGCGAGCC ATG GTG TTC TAT CGC GGC GTT TCT CTG CTG TCA AAG CTG 108
 Met Val Phe Tyr Arg Gly Val Ser Leu Leu Ser Lys Leu
 1 5 10
 CGT TCT CGA GCG GTC CAA CAG ACA AAT CTT AGC AAC TCT GTG CGG TGG 156
 Arg Ser Arg Ala Val Gln Gln Thr Asn Leu Ser Asn Ser Val Arg Trp
 15 20 25
 CTT CAA GTC CAA ACC TCT TCT GGT CTT GAT CTG CGT TCT GAG CTG CAA 204
 Leu Gln Val Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu Gln
 30 35 40 45
 GAA TTG ATT CCA GAA CAA CAG GAT CGC CTA AAG AAG CTC AAG TCA GAG 252
 Glu Leu Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Leu Lys Ser Glu
 50 55 60
 CAT GGA AAG GTT CAA TTG GGA AAC ATC ACA GTT GAT ATG GTT CTT GGT 300
 His Gly Lys Val Gln Leu Gly Asn Ile Thr Val Asp Met Val Leu Gly
 65 70 75

GGA ATG AGA GGA ATG ACA GGA TTA CTG TGG GAA ACC TCA TTA CTT GAC Gly Met Arg Gly Met Thr Gly Leu Leu Trp Glu Thr Ser Leu Leu Asp 80 85 90	348
CCC GAT GAA GGA ATT CGC TTT CGG GGC TTG TCT ATC TAT GAA TGC CAA Pro Asp Glu Gly Ile Arg Phe Arg Gly Leu Ser Ile Tyr Glu Cys Gln 95 100 105	396
AAG GTA TTA CCT GCA GCA AAG CCT GGG GGA GAG CCC TTG CCT GAA GGT Lys Val Leu Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu Gly 110 115 120 125	444
CTT CTC TGG CTT CTT TTA ACA GGA AAG GTG CCA TCA AAA GAG CAA GTG Leu Leu Trp Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val 130 135 140	492
GAT TCA TTG TCT CAG GAA TTG CGA AGT CGT GCT ACT GTC CCC GAT CAT Asp Ser Leu Ser Gln Glu Leu Arg Ser Arg Ala Thr Val Pro Asp His 145 150 155	540
GTA TAC AAA ACT ATT GAT GCC TTA CCA GTC ACA GCT CAT CCA ATG ACT Val Tyr Lys Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro Met Thr 160 165 170	588
CAG TTT GCT ACT GGA GTC ATG GCT CTT CAG GTT CAA AGT GAA TTT CAA Gln Phe Ala Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu Phe Gln 175 180 185	636
AAG GCA TAT GAG AAA GGG ATT CAC AAA TCA AAG TTA TGG GAA CCG ACA Lys Ala Tyr Glu Lys Gly Ile His Lys Ser Lys Leu Trp Glu Pro Thr 190 195 200 205	684
TAT GAG GAT TCC ATG AGT TTG ATT GCT CAA GTT CCA CTT GTT GCT GCT Tyr Glu Asp Ser Met Ser Leu Ile Ala Gln Val Pro Leu Val Ala Ala 210 215 220	732
TAT GTT TAT CGC AGG ATG TAC AAG AAC GGC AAC ACT ATA CCT AAG GAT Tyr Val Tyr Arg Arg Met Tyr Lys Asn Gly Asn Thr Ile Pro Lys Asp 225 230 235	780
GAC TCA CTG GAT TAT GGT GCA AAT TTT GCT CAC ATG CTT GGT TTC AGT Asp Ser Leu Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly Phe Ser 240 245 250	828
AGC TCT GAC ATG CAT GAG CTT ATG AAG CTC TAT GTC ACG ATA CAC AGT Ser Ser Asp Met His Glu Leu Met Lys Leu Tyr Val Thr Ile His Ser 255 260 265	876
GAT CAT GAA GGT GGT AAC GTC AGT GCT CAC ACA GGT CAC TTG GTT GCT Asp His Glu Gly Gly Asn Val Ser Ala His Thr Gly His Leu Val Ala 270 275 280 285	924
AGT GCT TTG TCA GAC CCT TAC CTC TCC TTC GCT GCT GCT TTG AAT GGT Ser Ala Leu Ser Asp Pro Tyr Leu Ser Phe Ala Ala Ala Leu Asn Gly 290 295 300	972
TTA GCT GGA CCA CTT CAT GGT TTA GCC AAT CAG GAA GTT TTG CTA TGG Leu Ala Gly Pro Leu His Gly Leu Ala Asn Gln Glu Val Leu Leu Trp 305 310 315	1020

ATC AAA TCT GTT GTA GAG GAG TGT GGG GAG AAC ATT TCC AAA GAG CAG Ile Lys Ser Val Val Glu Glu Cys Gly Glu Asn Ile Ser Lys Glu Gln 320 325 330	1068
TTG AAA GAC TAC GCT TGG AAA ACA TTG AAA AGT GGC AAG GTT GTC CCT Leu Lys Asp Tyr Ala Trp Lys Thr Leu Lys Ser Gly Lys Val Val Pro 335 340 345	1116
GGT TTC GGA CAT GGA GTT CTG CGC AAG ACT GAT CCA AGA TAC ACA TGC Gly Phe Gly His Gly Val Leu Arg Lys Thr Asp Pro Arg Tyr Thr Cys 350 355 360 365	1164
CAG AGA GAG TTC GCT TTG AAG CAT TTG CCT GAA GAT CCA CTG TTT CAA Gln Arg Glu Phe Ala Leu Lys His Leu Pro Glu Asp Pro Leu Phe Gln 370 375 380	1212
CTG GTT GCA AAA CTC TAC GAA GTG TTC CTC CAA TTC TTA CAG AAC TTG Leu Val Ala Lys Leu Tyr Glu Val Phe Leu Gln Phe Leu Gln Asn Leu 385 390 395	1260
GCA AAG TTA AAC CCT TGG CCA AAT GTT GAT GCC CAC AGT GGT GTG TTG Ala Lys Leu Asn Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu 400 405 410	1308
TTG AAC TAT TAT GGT TTA ACT GAA GCA AGA TAT TAT ACG GTC CTC TTT Leu Asn Tyr Tyr Gly Leu Thr Glu Ala Arg Tyr Tyr Thr Val Leu Phe 415 420 425	1356
GGT GTA TCA AGA GCT CTT GGC ATT TGC TCT CAG CTA ATT TGG GAC CGA Gly Val Ser Arg Ala Leu Gly Ile Cys Ser Gln Leu Ile Trp Asp Arg 430 435 440 445	1404
GCT CTT GGA TTG CCA CTA GAG AGG CCA AAG AGT GTC ACA ATG GAG TGG Ala Leu Gly Leu Pro Leu Glu Arg Pro Lys Ser Val Thr Met Glu Trp 450 455 460	1452
CTT GAG AAC CAT TGC AAG AAA GCA TGATTTGTTT GAAATCTCTG CGAGCATAAA Leu Glu Asn His Cys Lys Lys Ala 465	1506
AGCACAATGT AAAATCTTTA TGAATAATTG CTTGAGAAAG CAGTTTTTTTC TTGGAGCCAA	1566
GGTAGGTGCGC ATTAGGATGT TCATCGATTG GCTTAGTACG GTTTTGAAAG ATTTTG GTTG	1626
TGTATTTTCA GTTTCGGTTT TAAAAATGTT ATACCAATAC CTTATCGATA TAAATTCAAT	1686
ATGATTCGAT TTTTACTTTT TGTTTGAAAA AAAAAACAAA AAAAAAAAAA AAAAAAAAAA	1746
A	1747

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Phe Tyr Arg Gly Val Ser Leu Leu Ser Lys Leu Arg Ser Arg
1 5 10 15

Ala Val Gln Gln Thr Asn Leu Ser Asn Ser Val Arg Trp Leu Gln Val
20 25 30

Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu Gln Glu Leu Ile
35 40 45

Pro Glu Gln Gln Asp Arg Leu Lys Lys Leu Lys Ser Glu His Gly Lys
50 55 60

Val Gln Leu Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Met Arg
65 70 75 80

Gly Met Thr Gly Leu Leu Trp Glu Thr Ser Leu Leu Asp Pro Asp Glu
85 90 95

Gly Ile Arg Phe Arg Gly Leu Ser Ile Tyr Glu Cys Gln Lys Val Leu
100 105 110

Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu Gly Leu Leu Trp
115 120 125

Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ser Leu
130 135 140

Ser Gln Glu Leu Arg Ser Arg Ala Thr Val Pro Asp His Val Tyr Lys
145 150 155 160

Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro Met Thr Gln Phe Ala
165 170 175

Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu Phe Gln Lys Ala Tyr
180 185 190

Glu Lys Gly Ile His Lys Ser Lys Leu Trp Glu Pro Thr Tyr Glu Asp
195 200 205

Ser Met Ser Leu Ile Ala Gln Val Pro Leu Val Ala Ala Tyr Val Tyr
210 215 220

Arg Arg Met Tyr Lys Asn Gly Asn Thr Ile Pro Lys Asp Asp Ser Leu
225 230 235 240

Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly Phe Ser Ser Ser Asp
245 250 255

Met His Glu Leu Met Lys Leu Tyr Val Thr Ile His Ser Asp His Glu
260 265 270

Gly Gly Asn Val Ser Ala His Thr Gly His Leu Val Ala Ser Ala Leu
275 280 285

Ser Asp Pro Tyr Leu Ser Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly
290 295 300

Pro Leu His Gly Leu Ala Asn Gln Glu Val Leu Leu Trp Ile Lys Ser
305 310 315 320

Val Val Glu Glu Cys Gly Glu Asn Ile Ser Lys Glu Gln Leu Lys Asp
325 330 335

Tyr Ala Trp Lys Thr Leu Lys Ser Gly Lys Val Val Pro Gly Phe Gly
340 345 350
His Gly Val Leu Arg Lys Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu
355 360 365
Phe Ala Leu Lys His Leu Pro Glu Asp Pro Leu Phe Gln Leu Val Ala
370 375 380
Lys Leu Tyr Glu Val Phe Leu Gln Phe Leu Gln Asn Leu Ala Lys Leu
385 390 395 400
Asn Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu Asn Tyr
405 410 415
Tyr Gly Leu Thr Glu Ala Arg Tyr Tyr Thr Val Leu Phe Gly Val Ser
420 425 430
Arg Ala Leu Gly Ile Cys Ser Gln Leu Ile Trp Asp Arg Ala Leu Gly
435 440 445
Leu Pro Leu Glu Arg Pro Lys Ser Val Thr Met Glu Trp Leu Glu Asn
450 455 460
His Cys Lys Lys Ala
465

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGGATCC ATGGTGT TTT TCCGCAGCGT AT

32

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATAGGATCC TTAAGCAGAT GAAGCTTCT TA

32

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCGGTACC ATGTACAGAT GCGCATCGTC T

31

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACGGATCC CTTGGTTGCA ACAGCAGCTG A

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAGGGATCC ATGTCAGCGA TATTATCAAC AACTAGCAAA AGT

43

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATTGGATCC TTAGTTCTTA CTTTCGATTT TCTTTACCAA CTC

43

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAGGGATCC ATGGCTGATA CAAAAGCAA

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATTGGATCC TTAACGCTTG ATATCGCTT

29